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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/893,737

DATE: 07/12/2001

TIME: 09:25:38

Input Set : A:\0041.txt

Output Set: N:\CRF3\07122001\I893737.raw

4 <110> APPLICANT: Sheppard, Paul O.
 5 Presnell, Scott R.
 7 <120> TITLE OF INVENTION: MAMMALIAN SECRETED PROTEINS
 9 <130> FILE REFERENCE: 00-41

C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/893,737

C--> 11 <141> CURRENT FILING DATE: 2001-06-28

11 <150> PRIOR APPLICATION NUMBER: US 60/215,446

12 <151> PRIOR FILING DATE: 2000-06-30

14 <160> NUMBER OF SEQ ID NOS: 329

16 <170> SOFTWARE: FastSEQ for Windows Version 3.0

18 <210> SEQ ID NO: 1

19 <211> LENGTH: 453

20 <212> TYPE: DNA

21 <213> ORGANISM: Homo sapiens

23 <220> FEATURE:

24 <221> NAME/KEY: CDS

25 <222> LOCATION: (1)...(453)

27 <400> SEQUENCE: 1

28	atg	ctc	ttc	cct	ggc	ctc	acc	act	acc	ctc	ctg	ctc	ctg	gtt	ttc	ttc	48
29	Met	Leu	Phe	Pro	Gly	Leu	Thr	Thr	Thr	Leu	Leu	Leu	Leu	Val	Phe	Phe	
30	1				5					10					15		
32	ctg	ctg	gtt	ttc	tcc	ctg	cct	gct	ggc	cta	cat	aca	gcc	ctc	aca	gca	96
33	Leu	Leu	Val	Phe	Ser	Leu	Pro	Ala	Gly	Leu	His	Thr	Ala	Leu	Thr	Ala	
34				20					25				30				
36	gcc	aga	gga	ctc	ccc	aaa	ctg	ccc	aag	cac	agc	cac	atc	gcc	aaa	gac	144
37	Ala	Arg	Gly	Leu	Pro	Lys	Leu	Pro	Lys	His	Ser	His	Ile	Ala	Lys	Asp	
38			35				40				45						
40	acc	cat	tca	tcc	ttc	cca	tct	cag	ctc	cag	ggg	ctg	ctt	tcc	aaa	gca	192
41	Thr	His	Ser	Ser	Phe	Pro	Ser	Gln	Leu	Gln	Gly	Leu	Leu	Ser	Lys	Ala	
42		50					55				60						
44	aca	cca	cat	aga	cat	ccc	tgt	gat	ata	gca	cag	ttc	aaa	act	gtg	cgc	240
45	Thr	Pro	His	Arg	His	Pro	Cys	Asp	Ile	Ala	Gln	Phe	Lys	Thr	Val	Arg	
46	65				70				75				80				
48	att	cag	gag	agc	cag	cag	cag	gtg	gtc	acc	aag	agg	aaa	ttc	cag	cac	288
49	Ile	Gln	Glu	Ser	Gln	Gln	Gln	Val	Val	Thr	Lys	Arg	Lys	Phe	Gln	His	
50				85				90					95				
52	ttc	aca	gcc	att	cac	agg	cag	ggc	tcc	tat	gtt	tat	caa	gac	aat	agg	336
53	Phe	Thr	Ala	Ile	His	Arg	Gln	Gly	Ser	Tyr	Val	Tyr	Gln	Asp	Asn	Arg	
54			100					105					110				
56	cgc	act	act	gaa	cat	aga	ccc	tca	tca	gcg	gtt	ttg	ctt	ttg	ccc	ttt	384
57	Arg	Thr	Thr	Glu	His	Arg	Pro	Ser	Ser	Ala	Val	Leu	Leu	Leu	Pro	Phe	
58			115				120				125						
60	gcc	ctg	ttt	cct	cag	aag	cat	gtg	atc	ttt	gtt	aga	ccc	tta	tca	gtg	432
61	Ala	Leu	Phe	Pro	Gln	Lys	His	Val	Ile	Phe	Val	Arg	Pro	Leu	Ser	Val	
62		130					135				140						
64	gtt	ctg	ctt	ttt	gca	ctt	tga										453
65	Val	Leu	Leu	Phe	Ala	Leu	*										

ENTERED

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66 145                               150
69 <210> SEQ ID NO: 2
70 <211> LENGTH: 150
71 <212> TYPE: PRT
72 <213> ORGANISM: Homo sapiens
74 <400> SEQUENCE: 2
75 Met Leu Phe Pro Gly Leu Thr Thr Thr Leu Leu Leu Leu Val Phe Phe
76 1                               5                               10                               15
77 Leu Leu Val Phe Ser Leu Pro Ala Gly Leu His Thr Ala Leu Thr Ala
78 20                               25                               30
79 Ala Arg Gly Leu Pro Lys Leu Pro Lys His Ser His Ile Ala Lys Asp
80 35                               40                               45
81 Thr His Ser Ser Phe Pro Ser Gln Leu Gln Gly Leu Leu Ser Lys Ala
82 50                               55                               60
83 Thr Pro His Arg His Pro Cys Asp Ile Ala Gln Phe Lys Thr Val Arg
84 65                               70                               75                               80
85 Ile Gln Glu Ser Gln Gln Gln Val Val Thr Lys Arg Lys Phe Gln His
86 85                               90                               95
87 Phe Thr Ala Ile His Arg Gln Gly Ser Tyr Val Tyr Gln Asp Asn Arg
88 100                              105                              110
89 Arg Thr Thr Glu His Arg Pro Ser Ser Ala Val Leu Leu Pro Phe
90 115                              120                              125
91 Ala Leu Phe Pro Gln Lys His Val Ile Phe Val Arg Pro Leu Ser Val
92 130                              135                              140
93 Val Leu Leu Phe Ala Leu
94 145                              150
96 <210> SEQ ID NO: 3
97 <211> LENGTH: 303
98 <212> TYPE: DNA
99 <213> ORGANISM: Homo sapiens
101 <220> FEATURE:
102 <221> NAME/KEY: CDS
103 <222> LOCATION: (1)...(303)
105 <400> SEQUENCE: 3
106 atg gaa atc ctt cac aat gaa atc tca gag ctg gaa tct ctc act ctc      48
107 Met Glu Ile Leu His Asn Glu Ile Ser Glu Leu Glu Ser Leu Thr Leu
108 1                               5                               10                               15
109 gtc cct ccc ctc atc ttc tta ctt tta ccc agc aga tct acc cgt ggg      96
110 Val Pro Pro Leu Ile Phe Leu Leu Leu Pro Ser Arg Ser Thr Arg Gly
111 20                               25                               30
112 cag ccc ttt tcc caa gta cca ggg gag aaa atg gat tca gaa aag gat      144
113 Gln Pro Phe Ser Gln Val Pro Gly Glu Lys Met Asp Ser Glu Lys Asp
114 35                               40                               45
115 ttg tgg gga gag gag ctt cca cac tta ata ctg aaa gag gct ttt cat      192
116 Leu Trp Gly Glu Glu Leu Pro His Leu Ile Leu Lys Glu Ala Phe His
117 50                               55                               60
118 ctg ttt ttc aag cca aca gca gcc cca ttc cca gat tca ctc aag gtc      240
119 Leu Phe Phe Lys Pro Thr Ala Ala Pro Phe Pro Asp Ser Leu Lys Val
120 65                               70                               75                               80
121
122
123
124

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126 tcc ctt aca tgt ccc tgg aaa gaa gga ggg tca cat aca aga tgc cag      288
127 Ser Leu Thr Cys Pro Trp Lys Glu Gly Gly Ser His Thr Arg Cys Gln
128                               85                               90                               95
130 agt ggc agc agg tga      303
131 Ser Gly Ser Arg *
132                               100
135 <210> SEQ ID NO: 4
136 <211> LENGTH: 100
137 <212> TYPE: PRT
138 <213> ORGANISM: Homo sapiens
140 <400> SEQUENCE: 4
141 Met Glu Ile Leu His Asn Glu Ile Ser Glu Leu Glu Ser Leu Thr Leu
142 1                               5                               10                               15
143 Val Pro Pro Leu Ile Phe Leu Leu Leu Pro Ser Arg Ser Thr Arg Gly
144                               20                               25                               30
145 Gln Pro Phe Ser Gln Val Pro Gly Glu Lys Met Asp Ser Glu Lys Asp
146                               35                               40                               45
147 Leu Trp Gly Glu Glu Leu Pro His Leu Ile Leu Lys Glu Ala Phe His
148                               50                               55                               60
149 Leu Phe Phe Lys Pro Thr Ala Ala Pro Phe Pro Asp Ser Leu Lys Val
150 65                               70                               75                               80
151 Ser Leu Thr Cys Pro Trp Lys Glu Gly Gly Ser His Thr Arg Cys Gln
152                               85                               90                               95
153 Ser Gly Ser Arg
154                               100
156 <210> SEQ ID NO: 5
157 <211> LENGTH: 276
158 <212> TYPE: DNA
159 <213> ORGANISM: Homo sapiens
161 <220> FEATURE:
162 <221> NAME/KEY: CDS
163 <222> LOCATION: (1)...(276)
165 <400> SEQUENCE: 5
166 atg agt ttg ctg ttg ctg ctg ctg ctg ctg ctg ctg ctg ctg ctg ctg      48
167 Met Ser Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu
168 1                               5                               10                               15
170 ctg ttt aaa tgg aaa aga aga gta gta agt ggt cat ctt ctc agc gtc      96
171 Leu Phe Lys Trp Lys Arg Arg Val Val Ser Gly His Leu Leu Ser Val
172                               20                               25                               30
174 tgg tgc tgg tcc cgc cca cac act gtg gca gag cag acc cac ctg ttg      144
175 Trp Cys Trp Ser Arg Pro His Thr Val Ala Glu Gln Thr His Leu Leu
176                               35                               40                               45
178 tca ctg gga aat gag ggg ctg cag gta ctg ccc tta gac aat gga ggt      192
179 Ser Leu Gly Asn Glu Gly Leu Gln Val Leu Pro Leu Asp Asn Gly Gly
180                               50                               55                               60
182 ggc caa gga cgt ttg ggg aca gat tac agg aaa gct caa caa ttc cct      240
183 Gly Gln Gly Arg Leu Gly Thr Asp Tyr Arg Lys Ala Gln Gln Phe Pro
184 65                               70                               75                               80
186 tca tgc ttt ggt gtt gag cac tgg cct cct ttt taa      276

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187 Ser Cys Phe Gly Val Glu His Trp Pro Pro Phe *
188                               85                               90
191 <210> SEQ ID NO: 6
192 <211> LENGTH: 91
193 <212> TYPE: PRT
194 <213> ORGANISM: Homo sapiens
196 <400> SEQUENCE: 6
197 Met Ser Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu
198 1                               5                               10                               15
199 Leu Phe Lys Trp Lys Arg Arg Val Val Ser Gly His Leu Leu Ser Val
200                               20                               25                               30
201 Trp Cys Trp Ser Arg Pro His Thr Val Ala Glu Gln Thr His Leu Leu
202                               35                               40                               45
203 Ser Leu Gly Asn Glu Gly Leu Gln Val Leu Pro Leu Asp Asn Gly Gly
204                               50                               55                               60
205 Gly Gln Gly Arg Leu Gly Thr Asp Tyr Arg Lys Ala Gln Gln Phe Pro
206 65                               70                               75                               80
207 Ser Cys Phe Gly Val Glu His Trp Pro Pro Phe
208                               85                               90
210 <210> SEQ ID NO: 7
211 <211> LENGTH: 591
212 <212> TYPE: DNA
213 <213> ORGANISM: Homo sapiens
215 <220> FEATURE:
216 <221> NAME/KEY: CDS
217 <222> LOCATION: (1)...(591)
219 <400> SEQUENCE: 7
220 atg agg ccg cga ggt ctc ccg ccg ctc ctg gtg gtg ctc ctg ggc tgc 48
221 Met Arg Pro Arg Gly Leu Pro Pro Leu Leu Val Val Leu Leu Gly Cys
222 1                               5                               10                               15
224 tgg gcc tcc gtg agc gcc cag acc gat gcc acc ccg gcg gtg acg aca 96
225 Trp Ala Ser Val Ser Ala Gln Thr Asp Ala Thr Pro Ala Val Thr Thr
226                               20                               25                               30
228 gag ggc ctc aac tcc acc gag gca gcc ctg gcc acc ttc gga act ttc 144
229 Glu Gly Leu Asn Ser Thr Glu Ala Ala Leu Ala Thr Phe Gly Thr Phe
230                               35                               40                               45
232 ccg tcg acc agg ccc ccc ggg act ccc agg gct cca ggg ccc tcc tcc 192
233 Pro Ser Thr Arg Pro Pro Gly Thr Pro Arg Ala Pro Gly Pro Ser Ser
234                               50                               55                               60
236 ggc ccc agg cct acc cca gtc acg gac gtt gct gtt ctc tgt gtc tgt 240
237 Gly Pro Arg Pro Thr Pro Val Thr Asp Val Ala Val Leu Cys Val Cys
238 65                               70                               75                               80
240 gac tta tcc cca gca cag tgt gac atc aac tgc tgc tgt gat ccc gac 288
241 Asp Leu Ser Pro Ala Gln Cys Asp Ile Asn Cys Cys Cys Asp Pro Asp
242                               85                               90                               95
244 tgc agc tcc gtg gat ttc agt gtc ttt tct gcc tgc tca gtt cca gtt 336
245 Cys Ser Ser Val Asp Phe Ser Val Phe Ser Ala Cys Ser Val Pro Val
246                               100                               105                               110
248 gtc aca ctt act gga gct ctc ccg tgt cag ctc gta gca cag aag gtg 384

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249 Val Thr Leu Thr Gly Ala Leu Pro Cys Gln Leu Val Ala Gln Lys Val
250      115      120      125
252 aag agc ctg ctg tgg ggc cag ggc ttc cca gat tac gtg gcc cct ttt      432
253 Lys Ser Leu Leu Trp Gly Gln Gly Phe Pro Asp Tyr Val Ala Pro Phe
254      130      135      140
256 gga aat tcc cag gcc cag gac atg ctg gac tgg tgc cca tcc act tca      480
257 Gly Asn Ser Gln Ala Gln Asp Met Leu Asp Trp Cys Pro Ser Thr Ser
258      145      150      155      160
260 tca ccc agt cat tca aca gga agg tgg tgt gat gaa ggc agc cgg gga      528
261 Ser Pro Ser His Ser Thr Gly Arg Trp Cys Asp Glu Gly Ser Arg Gly
262      165      170      175
264 agc cag ctg tta agg agg cag gat ggc cct gag tgg gag cgc ggg ctg      576
265 Ser Gln Leu Leu Arg Arg Gln Asp Gly Pro Glu Trp Glu Arg Gly Leu
266      180      185      190
268 aat ctt gga tac tga      591
269 Asn Leu Gly Tyr *
270      195
273 <210> SEQ ID NO: 8
274 <211> LENGTH: 196
275 <212> TYPE: PRT
276 <213> ORGANISM: Homo sapiens
278 <400> SEQUENCE: 8
279 Met Arg Pro Arg Gly Leu Pro Pro Leu Leu Val Val Leu Leu Gly Cys
280 1 5 10 15
281 Trp Ala Ser Val Ser Ala Gln Thr Asp Ala Thr Pro Ala Val Thr Thr
282 20 25 30
283 Glu Gly Leu Asn Ser Thr Glu Ala Ala Leu Ala Thr Phe Gly Thr Phe
284 35 40 45
285 Pro Ser Thr Arg Pro Pro Gly Thr Pro Arg Ala Pro Gly Pro Ser Ser
286 50 55 60
287 Gly Pro Arg Pro Thr Pro Val Thr Asp Val Ala Val Leu Cys Val Cys
288 65 70 75 80
289 Asp Leu Ser Pro Ala Gln Cys Asp Ile Asn Cys Cys Cys Asp Pro Asp
290 85 90 95
291 Cys Ser Ser Val Asp Phe Ser Val Phe Ser Ala Cys Ser Val Pro Val
292 100 105 110
293 Val Thr Leu Thr Gly Ala Leu Pro Cys Gln Leu Val Ala Gln Lys Val
294 115 120 125
295 Lys Ser Leu Leu Trp Gly Gln Gly Phe Pro Asp Tyr Val Ala Pro Phe
296 130 135 140
297 Gly Asn Ser Gln Ala Gln Asp Met Leu Asp Trp Cys Pro Ser Thr Ser
298 145 150 155 160
299 Ser Pro Ser His Ser Thr Gly Arg Trp Cys Asp Glu Gly Ser Arg Gly
300 165 170 175
301 Ser Gln Leu Leu Arg Arg Gln Asp Gly Pro Glu Trp Glu Arg Gly Leu
302 180 185 190
303 Asn Leu Gly Tyr
304 195
306 <210> SEQ ID NO: 9

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/893,737

DATE: 07/12/2001

TIME: 09:25:39

Input Set : A:\0041.txt

Output Set: N:\CRF3\07122001\I893737.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date